



SEQUENCE LISTING

<110> LAMBERT, Bart
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<120> New Bacillus Thuringiensis Strains and Their Insecticidal Proteins

<130> 2428-0125P

<140> New
<141> 2003-10-20

<150> US 09/220,806
<151> 1998-12-28

<150> US 08/379,656
<151> 1995-03-23

<160> 5

<170> PatentIn version 3.2

<210> 1
<211> 19
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> misc_feature
<222> (1)..(19)
<223> This probe is a part of the coding DNA strand of the cryIG gene, described by Smulevitch et al. (1991). This probe is used to isolate the bTS02618A gene from its containing strain.

<400> 1
ttctgtacta ttgattgta 19

<210> 2
<211> 1561
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> misc_feature
<222> (1)..(1561)
<223> Contains the translation initiation codon of the bTS02618A gene.

<400> 2
aaaaagaaat aggaataaat actatccatt ttttcaagaa atattttttt attagaaagg 60
aatctttctt acacgggaaa atcctaagat tgagagttaa gatatatata tataaataca 120

ataaagagtt tgtcaggatt tttgaaagat atgatatgaa catgcactag atttatagta	180
taggaggaaa aagtatgaat cgaaataatc aaaatgaata tgaaattatt gatgcccccc	240
attgtgggtg tccatcagat gacgatgtga ggtatccttt ggcaagtgc ccaaatgcag	300
cgttacaaaa tatgaactat aaagattact tacaatgac agatgaggac tacactgatt	360
cttatataaa tectagttta tctattagt gtagagatgc agttcagact gcgcttactg	420
ttgttgggag aatactcggg gcttttaggtg ttccgttttc tggacaaata gtgagttttt	480
atcaattcct tttaaataca ctgtggccag ttaatgatac agctatatgg gaagctttca	540
tgcgacaggt ggaggaactt gtcaatcaac aaataacaga atttgcaaga aatcaggcac	600
ttgcaagatt gcaaggatta ggagactctt ttaatgtata tcaacgttcc cttcaaaatt	660
ggttggtgta tcgaaatgat acacgaaatt taagtgtgtg tcgtgctnaa tttatagctt	720
tagaccttga ttttgtaatt gctattccat tgtttgagc aaatggacag cagggtccat	780
tactgtcagt atatgcacaa gctgtgaatt tacatttgtt attattaaaa gatgcatctc	840
tttttggaga aggatgggga ttcacacagg gggaaatttc cacatattat gaccgtcaat	900
tggaactaac cgctaagtac actaattact gtgaaacttg gtataataca ggtttagatc	960
gtttaagagg aacaaatact gaaagttggt taagatatca tcaattccgt agagaaatga	1020
cttttagtgg attagatggt gtggcgctat ttccatatta tgatgtacga ctttatccaa	1080
cgggatcaaa cccacagctt acacgtgagg tatatacaga tccgattgta tttaatccac	1140
cagctaattg tggactttgc cgacgttggg gtactaatcc ctataatact ttttctgagc	1200
tcgaaaatgc cttcattcgc ccaccacatc tttttgatag gctgaatagc ttaacaatca	1260
gcagtaatcg atttccagtt tcatctaatt ttatggatta ttggtcagga catacgttac	1320
gccgtagtta tctgaacgat tcagcagtac aagaagatag ttatggccta attacaacca	1380
caagagcaac aattaatccc ggagttgatg gaacaaaccg catagagtca acggcagtag	1440
attttcgttc tgcattgata ggtatatatg gcgtgaatag agcttctttt gtcccaggag	1500
gcttgtttaa tggtagcact tctcctgcta atggaggatg tagagatctc tatgatacaa	1560
	1561

a

<210> 3
 <211> 1554
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> misc_feature
 <222> (1146)..(1148)
 <223> Presumed translational stop codon of bTS02618A gene.

<400> 3
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 gctatagact agatggattt gtgaagagta gtcaagattt agaaattgat ctcatccaac 120
 atcataaagt ccatcttgta aaaaatgtac cagataatct agtatctgat acttactcag 180
 atggttcttg cagcggaatc aaccgttggt atgaacagca tcaggtagat atgcagctag 240
 atgcggagca tcatccaatg gattgctgtg aagcggctca aacacatgag ttttcttcct 300
 atattaatac aggggatcta aatgcaagt tagatcaggg catttgggtt gtattaaaag 360
 ttcgaacaac agatgggtat gcgacgttag gaaatcttga attggttagag gttgggcat 420
 tatcgggtga atctctagaa cggaacaaa gagataatgc gaaatggaat gcagagctag 480
 gaagaaaacg tgcagaaata gatcgtgtgt atttagctgc gaaacaagca attaatcatc 540
 tgtttgtaga ctatcaagat caacaattaa atccagaaat tgggctagca gaaattaatg 600
 aagcttcaaa tcttgttagag tcaatttcgg gtgtatatag tgatacacta ttacagattc 660
 ctgggattaa ctacgaaatt tacacagagt tatccgatcg cttacaacaa gcacgtatc 720
 tgtatactgc tagaaatgcg gtgcaaaatg gagactttaa cagtggctca gatagttgga 780
 atacaactat ggatgcatcg gttcagcaag atggcaatat gcatttctta gttctttcgc 840
 attgggatgc acaagtttcc caacaattga gagtaaacc gaattgtaag tatgtcttac 900
 gtgtgacagc aagaaaagta ggaggcggag atggatacgt cacaatccga gatggcgctc 960
 atcaccaaga aactcttaca tttaatgcat gtgactacga tgtaaattgt acgtatgtca 1020
 atgacaattc gtatataaca gaagaagtgg tattctaccc agagacaaaa catatgtggg 1080
 tagaggtagag tgaatccgaa ggttcattct atatagacag tattgagttt attgaaacac 1140
 aagagtagaa gagggggatc ctaacgtata gcaactatga gaggatactc cgtacaaaca 1200
 aagattaaaa aaaggtaaaa tgaatagaac cccctactgg tagaaggacc gatagggggg 1260
 tcttacatga aaaaatgtag ctgtttacta aggtgtataa aaaacagcat atctgataga 1320
 aaaaagttag taccttataa agaaagaatt ccattcacag tttcggatc atataaataa 1380
 tgataggggt atccttctta ttacattat ttttcgcaat tatctcgacg ttcttcttct 1440
 cgctcacaat gatgatgatc atgacaacaa tcgcgtccat agcgaactct ttogatatta 1500

ataatatcta aactcgtgta gcagtcattt ccattttttt tgatccagta aata 1554

<210> 4
 <211> 4344
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> CDS
 <222> (668)..(4141)
 <223> Encompasses the entire sequence of SEQ ID NO:2: from nucleotide position 474 to 2034 in SEQ ID NO:4; also encompasses part of the sequence of SEQ ID NO:3: from nucleotide position 2994 to nucleotide position 4344 in SEQ ID NO:4; SEQ ID NO:3 shows additional nucleotides, located downstream (3') from the sequence shown in SEQ ID NO:4 (nucleotide position 1352 to nucleotide position 1554 in SEQ ID NO:3)

<400> 4
 gaattcgagc tcggtacctt ttcagtgtat cgtttccctt ccatcagggt ttcaaattga 60
 aaagccgaat gatttgaaac ttgtttacga tgtaagtcatt ttgtctatga cgaaagatac 120
 gtgtaaaaaa cgtattgaga ttgatgaatg tggacaagta gaaattgact tacaagtatt 180
 aaagattaag ggtgtccttt cttttatcgg aaatttctct attgaacctt ttctgtgtga 240
 aaacatgtat acaacgggtg atagagatcc gtctatttcc ttaagtttcc aagatacggg 300
 atatgtggac catattttta aatatagcgt ccaacaacta ccatattatg taattgatgg 360
 tgatcatatt caagtacgtg atttacaat caaactgatg aaagagaatc cgcaatctgc 420
 tcaagtatca ggtttgtttt gttttgtata tgagtaagaa ccgaagggtt gtaaaaaaga 480
 aataggaata aatactatcc attttttcaa gaaatatttt tttattagaa aggaatcttt 540
 cttacacggg aaaatcctaa gattgagagt aaagatatat atatataaat acaataaaga 600
 gtttgtcagg atttttgaaa gatattgatat gaacatgcac tagatttata gtataggagg 660
 aaaaagt atg aat cga aat aat caa aat gaa tat gaa att att gat gcc 709
 Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala
 1 5 10
 ccc cat tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca 757
 Pro His Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala
 15 20 25 30
 agt gac cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta 805
 Ser Asp Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu
 35 40 45
 caa atg aca gat gag gac tac act gat tct tat ata aat cct agt tta 853
 Gln Met Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu

50	55	60	
tct att agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg Ser Ile Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly 65 70 75			901
aga ata ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt Arg Ile Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser 80 85 90			949
ttt tat caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct Phe Tyr Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala 95 100 105 110			997
ata tgg gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa Ile Trp Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln 115 120 125			1045
ata aca gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta Ile Thr Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu 130 135 140			1093
gga gac tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct Gly Asp Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala 145 150 155			1141
gat cga aat gat aca cga aat tta agt gtt gtt cgt gct caa ttt ata Asp Arg Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile 160 165 170			1189
gct tta gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat Ala Leu Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn 175 180 185 190			1237
gga cag cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta Gly Gln Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu 195 200 205			1285
cat ttg tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga His Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly 210 215 220			1333
ttc aca cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta Phe Thr Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu 225 230 235			1381
acc gct aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta Thr Ala Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu 240 245 250			1429
gat cgt tta aga gga aca aat act gaa agt tgg tta aga tat cat caa Asp Arg Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln 255 260 265 270			1477
ttc cgt aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt Phe Arg Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe 275 280 285			1525

cca tat tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt Pro Tyr Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu 290 295 300	1573
aca cgt gag gta tat aca gat ccg att gta ttt aat cca cca gct aat Thr Arg Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn 305 310 315	1621
gtt gga ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct Val Gly Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser 320 325 330	1669
gag ctc gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg Glu Leu Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu 335 340 345 350	1717
aat agc tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt Asn Ser Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe 355 360 365	1765
atg gat tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat Met Asp Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp 370 375 380	1813
tca gca gta caa gaa gat agt tat ggc cta att aca acc aca aga gca Ser Ala Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala 385 390 395	1861
aca att aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca Thr Ile Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala 400 405 410	1909
gta gat ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct Val Asp Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala 415 420 425 430	1957
tct ttt gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat Ser Phe Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn 435 440 445	2005
gga gga tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat Gly Gly Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp 450 455 460	2053
gaa agt acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt Glu Ser Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe 465 470 475	2101
agc ttt caa act aat cag gct gga tct ata gct aat gca gga agt gta Ser Phe Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val 480 485 490	2149
cct act tat gtt tgg acc cgt cgt gat gtg gac ctt aat aat acg att Pro Thr Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile 495 500 505 510	2197

acc cca aat aga att aca caa tta cca ttg gta aag gca tct gca cct	2245
Thr Pro Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro	
515 520 525	
gtt tgc ggt act acg gtc tta aaa ggt cca gga ttt aca gga ggg ggt	2293
Val Ser Gly Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly	
530 535 540	
ata ctc cga aga aca act aat ggc aca ttt gga acg tta aga gta acg	2341
Ile Leu Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr	
545 550 555	
gtt aat tca cca tta aca caa caa tat cgc cta aga gtt cgt ttt gcc	2389
Val Asn Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala	
560 565 570	
tca aca gga aat ttc agt ata agg gta ctc cgt gga ggg gtt tct atc	2437
Ser Thr Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile	
575 580 585 590	
ggg gat gtt aga tta ggg agc aca atg aac aga ggg cag gaa cta act	2485
Gly Asp Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr	
595 600 605	
tac gaa tcc ttt ttc aca aga gag ttt act act act ggt ccg ttc aat	2533
Tyr Glu Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn	
610 615 620	
ccg cct ttt aca ttt aca caa gct caa gag att cta aca gtg aat gca	2581
Pro Pro Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala	
625 630 635	
gaa ggt gtt agc acc ggt ggt gaa tat tat ata gat aga att gaa att	2629
Glu Gly Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile	
640 645 650	
gtc cct gtg aat ccg gca cga gaa gcg gaa gag gat tta gaa gcg gcg	2677
Val Pro Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala	
655 660 665 670	
aag aaa gcg gtg gcg agc ttg ttt aca cgt aca agg gac gga tta cag	2725
Lys Lys Ala Val Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln	
675 680 685	
gta aat gtg aca gat tat caa gtg gac caa gcg gca aat tta gtg tca	2773
Val Asn Val Thr Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser	
690 695 700	
tgc tta tcc gat gaa caa tat ggg cat gac aaa aag atg tta ttg gaa	2821
Cys Leu Ser Asp Glu Gln Tyr Gly His Asp Lys Lys Met Leu Leu Glu	
705 710 715	
gcg gta aga gcg gca aaa cgc ctc agc cgc gaa cgc aac tta ctt caa	2869
Ala Val Arg Ala Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln	
720 725 730	
gat cca gat ttt aat aca atc aat agt aca gaa gag aat ggc tgg aag	2917

Asp	Pro	Asp	Phe	Asn	Thr	Ile	Asn	Ser	Thr	Glu	Glu	Asn	Gly	Trp	Lys		
735					740					745					750		
gca	agt	aac	ggt	gtt	act	att	agc	gag	ggc	ggt	cca	ttc	ttt	aaa	ggt		2965
Ala	Ser	Asn	Gly	Val	Thr	Ile	Ser	Glu	Gly	Gly	Pro	Phe	Phe	Lys	Gly		
			755					760						765			
cgt	gca	ctt	cag	tta	gca	agc	gca	aga	gaa	aat	tat	cca	aca	tac	att		3013
Arg	Ala	Leu	Gln	Leu	Ala	Ser	Ala	Arg	Glu	Asn	Tyr	Pro	Thr	Tyr	Ile		
			770					775					780				
tat	caa	aaa	gta	gat	gca	tcg	gtg	tta	aag	cct	tat	aca	cgc	tat	aga		3061
Tyr	Gln	Lys	Val	Asp	Ala	Ser	Val	Leu	Lys	Pro	Tyr	Thr	Arg	Tyr	Arg		
		785					790					795					
cta	gat	gga	ttt	gtg	aag	agt	agt	caa	gat	tta	gaa	att	gat	ctc	atc		3109
Leu	Asp	Gly	Phe	Val	Lys	Ser	Ser	Gln	Asp	Leu	Glu	Ile	Asp	Leu	Ile		
	800					805					810						
cac	cat	cat	aaa	gtc	cat	ctt	gta	aaa	aat	gta	cca	gat	aat	tta	gta		3157
His	His	His	Lys	Val	His	Leu	Val	Lys	Asn	Val	Pro	Asp	Asn	Leu	Val		
					820					825					830		
tct	gat	act	tac	tca	gat	ggg	tct	tgc	agc	gga	atc	aac	cgt	tgt	gat		3205
Ser	Asp	Thr	Tyr	Ser	Asp	Gly	Ser	Cys	Ser	Gly	Ile	Asn	Arg	Cys	Asp		
				835					840					845			
gaa	cag	cat	cag	gta	gat	atg	cag	cta	gat	gcg	gag	cat	cat	cca	atg		3253
Glu	Gln	His	Gln	Val	Asp	Met	Gln	Leu	Asp	Ala	Glu	His	His	Pro	Met		
			850					855					860				
gat	tgc	tgt	gaa	gcg	gct	caa	aca	cat	gag	ttt	tct	tcc	tat	att	aat		3301
Asp	Cys	Cys	Glu	Ala	Ala	Gln	Thr	His	Glu	Phe	Ser	Ser	Tyr	Ile	Asn		
		865				870						875					
aca	ggg	gat	cta	aat	gca	agt	gta	gat	cag	ggc	att	tgg	gtt	gta	tta		3349
Thr	Gly	Asp	Leu	Asn	Ala	Ser	Val	Asp	Gln	Gly	Ile	Trp	Val	Val	Leu		
	880					885					890						
aaa	gtt	cga	aca	aca	gat	ggg	tat	gcg	acg	tta	gga	aat	ctt	gaa	ttg		3397
Lys	Val	Arg	Thr	Thr	Asp	Gly	Tyr	Ala	Thr	Leu	Gly	Asn	Leu	Glu	Leu		
	895				900					905					910		
gta	gag	gtt	ggg	cca	tta	tcg	ggg	gaa	tct	cta	gaa	cgg	gaa	caa	aga		3445
Val	Glu	Val	Gly	Pro	Leu	Ser	Gly	Glu	Ser	Leu	Glu	Arg	Glu	Gln	Arg		
			915					920						925			
gat	aat	gcg	aaa	tgg	aat	gca	gag	cta	gga	aga	aaa	cgt	gca	gaa	ata		3493
Asp	Asn	Ala	Lys	Trp	Asn	Ala	Glu	Leu	Gly	Arg	Lys	Arg	Ala	Glu	Ile		
			930					935					940				
gat	cgt	gtg	tat	tta	gct	gcg	aaa	caa	gca	att	aat	cat	ctg	ttt	gta		3541
Asp	Arg	Val	Tyr	Leu	Ala	Ala	Lys	Gln	Ala	Ile	Asn	His	Leu	Phe	Val		
		945					950					955					
gac	tat	caa	gat	caa	caa	tta	aat	cca	gaa	att	ggg	cta	gca	gaa	att		3589
Asp	Tyr	Gln	Asp	Gln	Gln	Leu	Asn	Pro	Glu	Ile	Gly	Leu	Ala	Glu	Ile		

960

965

970

aat gaa gct tca aat ctt gta gag tca att tcg ggt gta tat agt gat 3637
 Asn Glu Ala Ser Asn Leu Val Glu Ser Ile Ser Gly Val Tyr Ser Asp
 975 980 985 990

aca cta tta cag att cct ggg att aac tac gaa att tac aca gag tta 3685
 Thr Leu Leu Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu
 995 1000 1005

tcc gat cgc tta caa caa gca tcg tat ctg tat acg tct aga aat 3730
 Ser Asp Arg Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn
 1010 1015 1020

gcg gtg caa aat gga gac ttt aac agt ggt cta gat agt tgg aat 3775
 Ala Val Gln Asn Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn
 1025 1030 1035

aca act atg gat gca tcg gtt cag caa gat ggc aat atg cat ttc 3820
 Thr Thr Met Asp Ala Ser Val Gln Gln Asp Gly Asn Met His Phe
 1040 1045 1050

tta gtt ctt tcg cat tgg gat gca caa gtt tcc caa caa ttg aga 3865
 Leu Val Leu Ser His Trp Asp Ala Gln Val Ser Gln Gln Leu Arg
 1055 1060 1065

gta aat ccg aat tgt aag tat gtc tta cgt gtg aca gca aga aaa 3910
 Val Asn Pro Asn Cys Lys Tyr Val Leu Arg Val Thr Ala Arg Lys
 1070 1075 1080

gta gga ggc gga gat gga tac gtc aca atc cga gat ggc gct cat 3955
 Val Gly Gly Gly Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His
 1085 1090 1095

cac caa gaa act ctt aca ttt aat gca tgt gac tac gat gta aat 4000
 His Gln Glu Thr Leu Thr Phe Asn Ala Cys Asp Tyr Asp Val Asn
 1100 1105 1110

ggg acg tat gtc aat gac aat tcg tat ata aca gaa gaa gtg gta 4045
 Gly Thr Tyr Val Asn Asp Asn Ser Tyr Ile Thr Glu Glu Val Val
 1115 1120 1125

ttc tac cca gag aca aaa cat atg tgg gta gag gtg agt gaa tcc 4090
 Phe Tyr Pro Glu Thr Lys His Met Trp Val Glu Val Ser Glu Ser
 1130 1135 1140

gaa ggt tca ttc tat ata gac agt att gag ttt att gaa aca caa 4135
 Glu Gly Ser Phe Tyr Ile Asp Ser Ile Glu Phe Ile Glu Thr Gln
 1145 1150 1155

gag tag aagaggggga tcctaacgta tagcaactat gagaggatac tccgtacaaa 4191
 Glu

caaagattaa aaaaaggtaa aatgaataga accccctact ggtagaagga ccgatagggg 4251

gttcttacat gaaaaaatgt agctgtttac taaggtgtat aaaaaacagc atatctgata 4311

gaaaaaagtg agtaccttat aaagaaagaa ttc

4344

<210> 5
<211> 1157
<212> PRT
<213> Bacillus thuringiensis

<400> 5

Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Pro His
1 5 10 15

Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala Ser Asp
20 25 30

Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met
35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile
50 55 60

Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile
65 70 75 80

Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr
85 90 95

Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp
100 105 110

Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp
130 135 140

Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg
145 150 155 160

Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu
165 170 175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln
180 185 190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu
 195 200 205

Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr
 210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala
 225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg
 245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg
 260 265 270

Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr
 275 280 285

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg
 290 295 300

Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly
 305 310 315 320

Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu
 325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser
 340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp
 355 360 365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala
 370 375 380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile
 385 390 395 400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp
 405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe
 420 425 430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly
 435 440 445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser
 450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe
 465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr
 485 490 495

Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro
 500 505 510

Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser
 515 520 525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
 530 535 540

Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn
 545 550 555 560

Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr
 565 570 575

Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp
 580 585 590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
 595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro
 610 615 620

Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly
 625 630 635 640

Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro
645 650 655

Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys
660 665 670

Ala Val Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn
675 680 685

Val Thr Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu
690 695 700

Ser Asp Glu Gln Tyr Gly His Asp Lys Lys Met Leu Leu Glu Ala Val
705 710 715 720

Arg Ala Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro
725 730 735

Asp Phe Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser
740 745 750

Asn Gly Val Thr Ile Ser Glu Gly Gly Pro Phe Phe Lys Gly Arg Ala
755 760 765

Leu Gln Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln
770 775 780

Lys Val Asp Ala Ser Val Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp
785 790 795 800

Gly Phe Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His
805 810 815

His Lys Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp
820 825 830

Thr Tyr Ser Asp Gly Ser Cys Ser Gly Ile Asn Arg Cys Asp Glu Gln
835 840 845

His Gln Val Asp Met Gln Leu Asp Ala Glu His His Pro Met Asp Cys
850 855 860

Cys Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asn Thr Gly

865

870

875

880

Asp Leu Asn Ala Ser Val Asp Gln Gly Ile Trp Val Val Leu Lys Val
885 890 895

Arg Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu
900 905 910

Val Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn
915 920 925

Ala Lys Trp Asn Ala Glu Leu Gly Arg Lys Arg Ala Glu Ile Asp Arg
930 935 940

Val Tyr Leu Ala Ala Lys Gln Ala Ile Asn His Leu Phe Val Asp Tyr
945 950 955 960

Gln Asp Gln Gln Leu Asn Pro Glu Ile Gly Leu Ala Glu Ile Asn Glu
965 970 975

Ala Ser Asn Leu Val Glu Ser Ile Ser Gly Val Tyr Ser Asp Thr Leu
980 985 990

Leu Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asp
995 1000 1005

Arg Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val
1010 1015 1020

Gln Asn Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn Thr Thr
1025 1030 1035

Met Asp Ala Ser Val Gln Gln Asp Gly Asn Met His Phe Leu Val
1040 1045 1050

Leu Ser His Trp Asp Ala Gln Val Ser Gln Gln Leu Arg Val Asn
1055 1060 1065

Pro Asn Cys Lys Tyr Val Leu Arg Val Thr Ala Arg Lys Val Gly
1070 1075 1080

Gly Gly Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His His Gln
1085 1090 1095

Glu Thr Leu Thr Phe Asn Ala Cys Asp Tyr Asp Val Asn Gly Thr
1100 1105 1110

Tyr Val Asn Asp Asn Ser Tyr Ile Thr Glu Glu Val Val Phe Tyr
1115 1120 1125

Pro Glu Thr Lys His Met Trp Val Glu Val Ser Glu Ser Glu Gly
1130 1135 1140

Ser Phe Tyr Ile Asp Ser Ile Glu Phe Ile Glu Thr Gln Glu
1145 1150 1155